

09988745-112001

10 30 50
CTAGAGCTAGCAGGAGTAACTCTCATGGAACCTTGGAACCATTTCTTCAATTGAATTTCA
70 90 110
GGGCACATTTGAATCAGTACCCAGGGGCACTGTACTATGCTCCCAGCTGGACCTTAGTTT
130 150 170
CCTCCTCCTCGTTTCACCTGTGAGTAATTAACAGACAAAATTTTTTTTTTTTTTTTTT
190 210 230
TTTTTTTTTTTTTTTGGCCCTCCAGTGGAGAAGGTGGCCAGTTCTCAGACAGAGGAAGAGT
250 270 290
AGAAATCATAAATGAGAGCTGTCTTCATCCAAGGTGCTGAAGAGCACCTGCGGCATTCT
M R A V F I Q G A E E H P A A F C 17
310 330 350
GCTACCAGGTGAATGGGTCTTGCCCCAGGACAGTACATACTCTGGGCATCCAGTTGGTCA
Y Q V N G S C P R T V H T L S I Q L V I
370 390 410
TCTACCTGACCTGTGCAGCAGGCATGCTGATTATCGTGCTAGGGAATGTATTTGTGGCAT
Y L T C A A G M L I I V L G N V F V A F
430 450 470
TTGCTGTGTCTTACTTCAAAGCGCTTCACACGCCCACCAACTTCCTGCTGCTCTCCCTGG
A V S Y F K A L H T P T N F L L L S L A
490 510 530
CCCTGGCTGACATGTTTCTGGGTCTGCTGGTGTGCCCCCTCAGCACCATTCGCTCAGTGG
L A D M F L G L L V L P L S T I R S V E
550 570 590
AGAGCTGCTGGTTCTTCGGGGACTTCCTCTGCCGCTGCACACCTACCTGGACACCCTCT
S C W F F G D F L C R L H T Y L D T L F
610 630 650
TCTGCCTCACCTCCATCTTCCATCTCTGTTTCATTTCCATTGACCGCCACTGTGCCATCT
C L T S I F H L C F I S I D R H C A I C
670 690 710
GTGACCCCTGCTCTATCCCTCCAAGTTCACAGTGAGGGTGGCTCTCAGGTACATCCTGG
D P L L Y P S K F T V R V A L R Y I L A
730 750 770
CAGGATGGGGGGTGGCCGAGCATACTTCGTTATTCTCTACACAGATGTGGTAGAGA
G W G V P A A Y T S L F L Y T D V V E T
790 810 830
CAAGGCTCAGCCAGTGGCTGGAAGAGATGCCTTGTGTGGGCAGTTGCCAGCTGCTGCTCA
R L S Q W L E E M P C V G S C Q L L L N
850 870 890
ATAAATTTTGGGGCTGGTTAAACTTCCCTTTGTTCTTTGTCCCCTGCCTCATTATGATCA
K F W G W L N F P L F F V P C L I M I S 20
910 930 950
GCTTGTATGTGAAGATCTTTGTGGTTGCTACCAGACAGGCTCAGCAGATTACCACATTGA
L Y V K I F V V A T R Q A Q Q I T T L S
970 990 1010
GCAAAAGCCTGGCTGGGGCTGCCAAGCATGAGAGAAAAGCTGCCAAGACCCTGGGCATTG
K S L A G A A K H E R K A A K T L G I V
1030 1050 1070
TTGTGGGCATATACCTCTTGTGCTGGCTGCCCTTCACCATAGACACGATGGTCGACAGCC
V G I Y L L C W L P F T I D T M V D S L
1090 1110 1130
TCCTTCACTTTATCACACCCCCACTGGTCTTTGACATCTTTATCTGGTTTGCTTACTTCA
L H F I T P P L V F D I F I W F A Y F N
1150 1170 1190
ACTCAGCCTGCAACCCCATCATCTATGTCTTTTCTTACCAGTGGTTTCGGAAGGCACTGA
S A C N P I I Y V F S Y Q W F R K A L K 210
1210 1230 1250
AACTCACACTGAGCCAGAAGGTCTTCTACCGCAGACACGCACTGTTGATTTGTACCAAG
L T L S Q K V F S P Q T R T V D L Y Q E
1270 1290 1310
AATGATTCCTTCTACTAAATGCAGGCAAGGAGTAGGACCTCACAGGAAAGATAAGTGGA
*
1330 1350 1370
CTGTGACCGCGGGCTGTGTGGTGTGAGTTTGTGGGCATGCTTCCAGGACAGCATGGGT

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FIGURE

1 1/1

1013

Homology Comparison **HDGRC02 X Mu.β-1 Adrenoreceptor**

Percent Similarity: 55.864 Percent Identity: 32.099

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3 AVFIQGAEEHPAAFCYQVNGSCPRTVH.TLGIQLVIYLTCAAGMLIIVLG 51
| :: |...: . . :||. | . : | |::|:: | . :|::|::|
30 ARLLVLASPPASLLPPASEGSAPLSQQWTAGMGLLVALI....VLLIVVG 75

52 NVFVAFVSYFKALHTPTNFLLLSLALADMFLGLLVLPLSTIRSVESCWF 101
||:| .|:: . |:: ||:::|||| |:::|||||:|::: . | : |
76 NVLVIVAIKTPRLQTLTNLFIMSLASADLVMGLLVVFPGATIVVWGRWE 125

102 FGDFLCRLHTYLDTLFCLTSIFHLCFISIDRHCAICDPLLYPSKFTVRVA 151
:|.|::| | | :|. | . .|| | |.|.::| | . | |. | : |
126 YGSFFCELWTSVDVLCVTASIE TLCVIALDRYLAITSPFRYQSLLTRARA 175

152 LRYILAGWGVPAAYTSLFLYTDVVETRLSQWLEEMPCVG...SCQLLLNK 198
. : . |::| : : : : : : : . |...| . :|::: | :
176 RALVCTVWAISAL...VSFLPILMHWWRAESDEARRCYNDPKCCDFVTNR 222

199 FWGWLNFPL.FFVPCLIMISLYVKIFVVATRQAQQITTLSKSLAGA.... 243
:: . : :|::| || :|:::| | :|...|.. :::: | :
223 AYAIASSVVSFYVPLCIMA FVYLRVFREAQKQVKKIDSCERRFLGGPARP 272

244 .....AKHERKAAKTLGIVVGIY 261
| :|.|| |||||::|::
273 PSPEPSPSPGPPRPADSLANGRSSKRRPSRLVALREQKALKTLGIIMGVF 322

262 LLCWLPFTIDTMVDSLHFITPPLVFDIFIWFAYFNSACNPIIYVFSYQW 311
||||| ::::|...: : .|. :| :| |::| ||| |||||. | : :
323 TLCWLPFFLANVVKAFHRDLVPDRLFVFFNWLGYSANSAFNPIIYCRSPDF 372

312 FRKALKLTLSQKVFSPOTRTVD 333
: :| ::: . . |...
373 RKA FQRLLCARRAACRRRAAH 394

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FIGURE 2 1/1
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Homology Comparison **HDGRC02 X Hu. D2 receptor**

Percent Similarity: 58.333 Percent Identity: 32.000

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8  GAEHPAAFCYQVNGSCPRTVHTLGIQLVIYLTCAAGMLIIVLGNVVFVAF 57
   :.:. . . . . : . . . . . : . . . . . : . . . . . : . . . . .
10 DDDLERQNWSRPFNGSDGKADRPYNYATLLT..LLIAVIVFGNVLVCM 57

58 AVSYFKATHTPTNFFLLSLALADMFLGLLVPLSTIRSVESCWFFGDFLC 107
   ||| ||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
58 AVSREKALQTTTNYLIVSLAVADLLVATLVMPWVVYLEVVGGEWKFSRIHC 107

108 RLHTYLDTLFCLTSIFHLCFISIDRHCAICDPLLPSKFTVRVALRYILA 157
   :. : || :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
108 DIFVTLDVMMCTASILNLCAISIDRYTAVAMPMLYNTRYSSKRRVTVMIS 157

158 .GWGVPAAYTSLFLYTDVVETRLSQWLEEMPCVGSQOLLNKFVGWLNFP 206
   .| :. . . . : :| :. . . . : :| :. . . . : :| :. . . . : :|
158 IVVWLSFTISCPLLFG.....LNNADQNECIIANPAFVV.....YSSIV 196

207 LFFVPCLIMISLYVKIFVVATRQAQQITT.....LSKSLAGAAKH 246
   | :| | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
197 SFYVPFIVTLLVYIKIYIVLRRRRKRVNTRKSSRAFRAHLRAPLKEAARR 246

247 .....ERKAAKTL 254
   | :| | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
297 EKNGHAKDHPKIAKIFEIQTMPNGKTRTSLKTMSRRKLSQQKEKKATQML 346

255 GIVVGIYLLCWL PFTIDTMVDSL LHFITPPLVFDIFIWFAYFNSACNP II 304
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
347 AIVLGVFIICWL PFFITHILNIHCDCNIPPVLYSAFTWLGYVNSAVNP II 396

305 YVFSYQWFRKALKLTL 320
   | . ||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
397 YTTFNIEFRKAFLKIL 412

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FIGURE 3
 325800-451 3 0 1 3